

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 22:43:10 ; Search time 4493 Seconds
(without alignments)
11192.889 Million cell updates/sec

Title: US-09-847-081b-1

Perfect score: 1728

Sequence: 1 agaaacccagagaagacaac.....tcatcaaacctcaagtgg 1728

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_pro:*
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12: gb_sy:*
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16: em_fun:*
17: em_hum:*
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22: em_ov:*
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27: em_sts:*
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40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862.8	49.9	1119	8	TOMPSY2A
2	856.2	49.5	1295	8	CAPSY1
3	847.6	49.1	1786	6	TOMCBPE
4	842	48.7	1646	6	A21360
5	842	48.7	1646	6	AR007503
6	829.8	48.0	1614	8	LERIPE
7	811.2	46.9	1239	6	A68204
8	811.2	46.9	1239	6	ARI56064
9	811.2	46.9	1239	6	BD005486
10	772	44.7	1355	8	LERYGTOM5
11	696.8	40.3	1506	8	AF220218
12	696.8	40.3	1589	8	AB037975
13	692.8	40.1	1773	8	AF152892
14	692.4	40.1	2868	6	E15683
15	678.4	39.3	1921	6	E15681
16	670.4	38.8	2085	6	E15680
17	653.4	37.8	1932	6	E15682
18	650.6	37.7	1637	8	HAN308385
19	645.8	37.4	1598	8	HAN304825
20	644.2	37.3	1371	6	AF251015
21	643.2	37.2	1372	6	A48337
22	643.2	37.2	1576	8	CMPSY1MR
23	625.4	36.2	1376	8	AY099482
24	591.6	34.2	1548	8	NPPSY
25	578.6	33.5	1703	8	AY085565
26	578.4	33.5	1853	8	AY056287
27	563.8	32.6	1769	8	ATHPHYSYN
28	514.2	29.8	1538	8	AB032797
29	512.2	29.6	1304	6	AX350858
30	463.8	26.8	1060	8	AY024350
31	426.4	24.7	686	8	AF158024
32	425	24.6	681	8	AF196963
33	415.2	24.0	1239	6	A68203
34	415.2	24.0	1239	6	ARI56063
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36	362.2	21.0	4073	8	LEPSPS
37	301.6	17.5	1278	8	DB091900
38	282.6	16.4	1859	8	AF305430
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40	252	14.6	1081	1	AB001284
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42	245	14.2	1465	1	SSPPHYSYN
43	245	14.2	119184	1	D90909
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ALIGNMENTS

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DEFINITION	Lycopersicon esculentum Mature leaf cDNA to mRNA.				
ACCESSION	L23424				
VERSION	L23424.1				
KEYWORDS	phytoene synthase				
SOURCE	Lycopersicon esculentum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.				
REFERENCE	1 (bases 1 to 1119)				

Pred. No. is the number of results predicted by chance to have a

AUTHORS Bartley G.E. and Scolnik, P.A.
 TITLE cDNA cloning, expression during development, and genome mapping of
 PSY2, a second tomato gene encoding phytoene synthase
 J. Biol. Chem. 268 (34), 25718-25721 (1993)
 MEDLINE 94064645
 PUBMED 8245008
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 QY 693 TGGCAGATATGTCAGAGATATCAAGACATTTTACTTAGGAACCAAGCTAATGACCCC 752
 DB 61 TGCGAAGATATGTCAGAGATATCAAGACATTTTACTTAGGAACCAAGCTAATGACCTC 120
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 DB 241 GGAAGATATTTTTCAGTGGGGCCATTTGATATGCTTGATGCTGCTTTATCCGATACTGT 300
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 LOCUS C.annuum psy1 mRNA for phytoene synthase. 1295 bp mRNA linear PLN 05-FEB-1994
 DEFINITION X68017
 ACCESSION X68017.1 GI:433993
 VERSION phytoene synthase.
 KEYWORDS Capsicum annum.
 SOURCE Capsicum annum.
 ORGANISM Capsicum annum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
 Kuntz, M.
 Direct Submission
 Submitted (30-JUL-1992) M. Kuntz, Inst. de Biologie Molec. des Plantes, 12 rue du Général Zimmer, 67084 Strasbourg, FRANCE
 2 (bases 1 to 1295)
 REFERENCE
 ROMER, S., HUGUENY, P., BOUVIER, F., CAMARA, B. and KUNTZ, M.
 Expression of the genes encoding the early carotenoid biosynthetic enzymes in Capsicum annum
 Biochem. Biophys. Res. Commun. 196 (3), 1414-1421 (1993)
 94071905
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 1..1295
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Best Local Similarity 81.5%; Pred. No. 4.8e-201;
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Db 1 ATGTCCTCTTCTGTTGGTGGTGTTCCTCCACCTTCCGAGGCTCGATGGGACAGGA 57

QY 310 TTGTTGGATTTCAGTCCGAGGAAGAACCGCGTCTTTGTATCATCCAGGTTCCCTAGTCGA 369
Db 58 TTCTTGGTATCCGTTCTGAGGGAACCGGATTTTGTATCGTCGCGG----- 105

QY 370 GATAGGAATTTGATGGGAATCAAGA---AGGTGGGAGACAAAGTGGGAAT 426
Db 106 CGTAGGAATTTGGCGTGCAATGAGAGAATCAAGAGAGGAGGTGGAACAAAGGTGGAGT 165

QY 427 TTTGGCTTTAATGCTGATCCAGATATATCATGCTTGGTGGATCAAGAACTGAAAG 486
Db 166 TTTGG-----TTCTTACTTGGGAGGACCAAACTGGAAGT 201

QY 487 GGAAGCACTTCTCTACAGTCCAGTTGGTGGCTAGCCAGCTGGAGAAATGACTGTG 546
Db 202 GGACGGAATTTCTGATCGTTCTGCTATCGTGGCTACTCGGCTGGAGAAATGACGATG 261

QY 547 TCATCAGAGAAAAGGTGATGATGTTGATTAAGCAGGCGAGCTTTAGTGAAGAGGACG 606
Db 262 TCATCAGAAACGGATGATGATGTTGTTTGGAGCAGGCGAGCTTTGGTGAAGAGACAG 321

QY 607 CTGAGACTACCGATGATTAGAGTGAAGCCGATATTTGTTCCAGGGAATTTGGGC 666
Db 322 CTGAGACTGAGGATGATGATGTTGTTGAGAGGATATACCTATTTCCGGGACTTTGGGC 381

QY 667 TTGTTGAGTGAAGCATATGATCGTTGTTGGCAAGTATGTGAGAGTATGCAAGACATTT 726
Db 382 TTGTTGAGTGAAGCATATGATGTTGTTGAGTATGTGAGAGTATGCGAGAGTACGCAAGC 441

QY 727 TACTTAGAACCAAGCTAATGACCCAGAGAGAGAGAGATCTCTGGCCAAATATATGTG 786
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QY 787 TGGTGCAGGAACCGATGATGTTGATGCGCTTATGATGCCCTATGATCCCATCACTCCGCA 846
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QY 907 CTTGATGCTGCTTATCCGATACCTGCTCCAGATTTCTCTGTTGATATTCAGCCATTCAGA 966

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VERSION
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M84744.1
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fruit stage fruit cDNA to mRNA.
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1. (bases 1 to 1786)
Barley, G.E., Viitanen, P.V., Bacot, K.O. and Scolnik, P.A.
A tomato gene expressed during fruit ripening encodes an enzyme of
the carotenoid biosynthesis pathway
J. Biol. Chem. 267 (8), 5036-5039 (1992)
92184738
PUBMED
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DB 447 TCAATAGAGGT----- 457
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DB 1410 TACTAGATGAGATTGAAGCAATGACTACAACTTCAACAGAGAGCATATGTGAGCA 1469
QY 1478 AGCCAAGAGAGTCTCTACCTTGCCTTATGCTTATGCAAAATCTTTGCCCCCTAATA 1537
DB 1470 AATCAAGAGAGTTGATTGTCATTACCTATTGCATATGCAAAATCTCTTGTGCTCTCTCAA 1529
QY 1538 GAATTCCTCTCCACTAGCAAGA 1561
DB 1530 AACTGCTCTCTTCAAGATAAA 1553
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RESULT 4
A21360 LOCUS A21360 1646 bp mRNA linear PAT 06-JUN-1994
DEFINITION L.esculentum pTOM5 mRNA.
ACCESSION A21360
VERSION A21360.1 GI:512395
KEYWORDS
SOURCE Lycopersicon esculentum.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
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            /note="involved in the carotenoid pathway"
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            /protein_id="CAA01548.1"
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/db_ref="SWISS-PROT:P08196"
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DELVDGPNASYITPAALDRWENLEDVFNGRFMDLGLSSTVSNFVDIOPFDMDI
EGRMDLRKSRITKNEDELILICYIVAGTVGLMSVPIMGITAPESKATTESVYNALALG
IANQLTNILRDVGEARRRVYLPODELAQGLSDEIDFAGVTPDKWIRFMKQIHRA
RRFDEAERGVTLSASRPVWASLVLYRKILDETEANDYNNFTKRAYVSKQVDC
IYICKISCASVKTASLOR"
polya_site 1630

BASE COUNT 529 a 249 c 388 g 480 t
ORIGIN

Query Match 48.7%; Score 842; DB 6; Length 1646;
Best Local Similarity 74.3%; Pred. No. 1.5e-197;
Matches 1222; Conservative 0; Mismatches 330; Indels 92; Gaps 9;

QY 101 TATAATCGTTGAATATAGTGGATAGACTCTAGTGGATATCTAC---AAGTATTGGTTTT 157
DB 53 TAAATTTTGTAGAGTGGAAATATCTCTAGTGGAAATCTACTAGGAGTAATTTATTT 112
QY 158 TGATAAAATAGGCTGAGTGGAGGTAACATAAAGGAGAGACAAACAACTTGGCAATTGT 217
DB 113 CTATAAACTAAGTAAGTTGGAGAGTGACA-AAAGAGAGACAAAAATCTTGGAAATGT 171
QY 218 TTTAGACCCAGGTTTCTTGTTCATGAGCATGCTGTTGCTTTGTTGCTGGTTGTTT 277
DB 172 TTTAGACAACCAAGT---TTTCTTGTCTAGATGCTGTTGCTTGTATGGTTGTTT 228
QY 278 CTCCCATCTCCGAGTCTCAATGGGACAGGATTTGGATTCAGTCCGAGAGAGAAACC. 337
DB 229 CTC---CTTGTGAGCTCAATGGGACAAAGTTTCATGGAATCAGTCCGGGAGGAAACC 285
QY 338 GCGTCTTTGATCATCCAGGTTCTAGCTCAGATAGGAATTCAGTGGAAATGGGAGAA 397
DB 286 GTTTTGTGATTCACGAGG-----CATAGGAATTTGGTGTCCAAATGAGAGAA 333
QY 398 TCAAGAAAGTGGGAGACAAAGGTGGAAATTTGGCTCTTTAATGCTGATCCCAAGATAT 457
DB 334 TCAATAGAGT----- 344
QY 458 CATGCTTGGTGGATCAAGAACTGAAAGGAGACACTTCTCTGTACATCCAGTTGG 517
DB 345 -----GGTGAAGACAACTAATAATGGACGGAATTTCTGTACGGTCTGCTATTT 396
QY 518 TGGCTAGCCAGCTGGGAGAAATGACTGTGCATCAGAGAAAAGGTGTATGATGTGTAT 577
DB 397 TGGCTACTCCATCTGGAGAACGGACGATGACATCGGACAGATGGTCTATGATGTGGTTT 456
QY 578 TAAAGCAGGACGCTTTAGTGAAGGACGCTGAGATCTACCGATGATTTAGAAGTGAAGC 637
DB 457 TGAGGAGGACGCTTGGTGAAGGACCACTGAGATCTACCAATGAGTTAGAGTGAAGC 516
QY 638 CGGATATTTGTTCCAGGAAATTTGGGCTTTGTGAGTGAAGCATATGATGTTGGCG 697
DB 517 CGGATATACCTATTTCCGGGAAATTTGGGCTTTGTGAGTGAAGCATATGATGAGTGTGGT 576
QY 698 AAGTATGTCAGAGTATGCAAGACATTTTACTTAGGAACCAAGCTAATGACCCACAGAGA 757
DB 577 AAGTATGTCAGAGTATGCAAGACGTTTAACTTAGGAACATATGCTAATGACTCCCGAGA 636
QY 758 GAAGAAGAGTATCTGGGCAATATATGTGGTGCAGAGAGACGGATGAGCTTTGTTGATG 817
DB 637 GAAGAAGGCTATCTGGCAATATATCTATGGTGCAGAGACAGATGAATGTTGATG 696
QY 818 GCCCTATGATCCCATACCTCCGCAAGCTTTAGATAGTGGGAGACACGCTGGAAG 877
DB 697 GCCCAACGCTATATATTTACCCCGACGCTTAGATAGTGGGAAATAGGCTAGAAG 756
QY 878 ATATTTTCACTGGGCGCCATTTGATATGCTGATGCTTTATCCGATACCTGCTCCA 937
DB 757 ATGTTTTCAATGGGCGCCCAATTTGACATGCTCGATGGTGTCTTGTCCGATACAGTTCTTA 816

QY 938 GATTTCCTGTGTATATTCAGCCATTTCAGATATGATTGAAGGAATCGTATGACTTGT 997
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QY 998 GGAATCCAGATCAAAACTTTTCGATGAGCTATATCTCTATTGTACTATTTGCTGGTA 1057
DB 877 GAAATTCAGATCAAAACTTCGACGAACATATACCTTTATTGTATTATTTGCTGGTA 936
QY 1058 CTCTAGATGATGATGCTTCCAGTATTGGTATTGCTGACCTGAATCAAGGCAACAACAG 1117
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QY 1118 AGAGTGTATATAATGCTGCTTTTGGCTTTAGGGCTTGCATAACTCAACCAATATACTCA 1177
DB 997 AGAGCTATATAATGCTGCTTTGCTCTGGGATCGCAAACTCAATTAACCTAATCTCA 1056
QY 1178 GAGATGATGAGAGATGCGCAGAGAGAGATATCTTCCCTCAAGATGAATTAGCAC 1237
DB 1057 GAGATGTTGGAGAGATGCGCAGAGAGAGAGTCTACTTGGCTCAAGATGAATTAGCAC 1116
QY 1238 AGCAGGCTCTCCGACGAGACATATTTGCTGGAAGAGTGCATGAATGGGGAAT 1297
DB 1117 AGCAGGCTCTCCGATGAGATATATTTGCTGGAAGGGTGACCGATAAATGGGAAATCT 1176
QY 1298 TTATGAAGAAACAAATTCAGAGGCGAGGAAATTTCTTTGATGAGTCAGAGAAAGTGTCA 1357
DB 1177 TTATGAAGAAACAAATACATAGGCGAGAAAGTCTTTGATGAGGAGAGAAAGCGTGA 1236
QY 1358 CAGAACTGAGCTGTGCTAGTAGAGTGGCTGTGTTAAAGCGCTGCTGTGTTATCGCAAGA 1417
DB 1237 CAGAAATGAGCTCAGCTAGTAGATTCCTGTATGGGATCTTTGCTCTTTGACCGCAAAA 1296
QY 1418 TATTGGACGAGATGGAAGCCAAACACTACACAACTTCACAAAGGAGGCTTATGTAGCA 1477
DB 1297 TACTAGATGAGATTGAAGCCAAATGACTACAACTTCACAAAGAGAGCATATGTGAGCA 1356
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QY 1537 AGAATTCCTCTCCACTAGCAAGACATGAATGAAGTAGTTGAGTCAATGATATATATAC 1596
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QY 1597 ACT-----AAGAAACTCAGTACTTGTAAATGAGATATCTTTGCTAAATGCTGAT 1648
DB 1477 AATGATCATTAGAAGAAAAAAGGAAGAAATGTTGTTGATGATATATATATATATAT 1536
QY 1649 CATCAAAAGTAGATTGT-----AAATTCATATGACAATCTCTTGTAGAATATTTCTCC 1704
DB 1537 CATAAATATTAGTTGTAGTAACATTCATATATATATATATCTCTTGTAGTTGTTGATCTTC 1596
QY 1705 AACTCATCAACCTCAAGTGAG 1728
DB 1597 ACTTATCTCAACTCTTTTGAGAG 1620

RESULT 5
AR007503
LOCUS AR007503 1646 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5750865.
ACCESSION AR007503
VERSION AR007503.1 GI:3966987
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1646)
AUTHORS Bird,C.Roger., Grierson,D. and Schuch,W.Walter.
TITLE Process for modifying the production of carotenoids in plants, and
DNA, constructs and cells therefor
JOURNAL Patent: US 5750865-A 2 12-MAY-1998;

FEATURES	Location/Qualifiers	
source	1..1646	
BASE COUNT	529 a 249 c 388 g 480 t	
ORIGIN		
 Query Match 48.7%; Score 842; DB 6; Length 1646; Best Local Similarity 74.3%; Pred. No. 1.5e-197; Matches 1222; Conservative 0; Mismatches 330; Indels 92; Gaps 9;		
QY	101 TATAATCTGTGAATTAGTGGTAGACTCTAGTGCGATATCTAC---	157 ---AAGTATTGGTTTT
DB	53 TAATTTGTTGAGAGTGGAAATATCTCTAGTGGGAATCTACTAGGAGTAATTTATTT	112
QY	158 TGATAAATAGGCTGAGGTGAGAGGTGAACAATAAGGAAAGAACAAAACTTGGGAATTGT	217
DB	113 CTATAAACTAAGTAAAGTTTGGAGGTGCACA-AAAAGAAGACAAAAATCTTGGAAATTGT	171
QY	218 TTATAGACCAGGAGTTTCCTGTTTCATGAGCATGCTCTGTTGCTTTGTTGGGTTGTTT	277
DB	172 TTATAGAACCAAGGT---TTTCTGTGCTAGAATGCTGTGTCCTTGTATGGGTTGTT	228
QY	278 CTCCTCCTCCGAGTCTCGAATGGGACAGATGTTGGATTTCAGTCCGAGAAAGAAC	337
DB	229 CTC---CTTGTGAGCTCTCAAATGGGCAAGTTTCATGGAATAGTCCGGGAGGGAAC	285
QY	338 CGCTCTTTGTATCATCCAGGTTCTTAGCTCGAGATAGGAATTTGATGGAATGGGAGAA	397
DB	286 GTTTTTTTGATTCATCGAG-----CATAGGAATTTGGTCCNATGAGAGAA	333
QY	398 TCAGAAGAGGTGGGAGACAAAGGTGGAAATTTTGCTCTTTAATTTGCTGATCCAAGATATT	457
DB	334 TCAATAGAGGT-----	344
QY	458 CATGCTTTGGTGGTAGACACTGAAAGGGAACACTTTCTCTGTACAGTCCAGTTGG	517
DB	345 -----GGTGGAAAGCAAACTAATATGAGCGGAATTTTGTACGGFTCTCTATTT	396
QY	518 TGGTAGCCCCAGCTGGGAGAAATGACTGTGTCATCAGAGAAAAAGGTGTATGATGGGTAT	577
DB	397 TGGCTACTCCATCTGGAGACGGACGTGACATCGGAACAGATGGTCTATGATGTGTTT	456
QY	578 TAAAGCAGGACGCTTTAGTGAAGAGGACGTGAGATCTACCGATGATTTAGAAGTGAAGC	637
DB	457 TGAGCGCAGGACGCTTGTGTAAGAGGCACTGAGATCTACCAATGAGTTAGAAGTGAAGC	516
QY	638 CGGATATTGTTGCCAGGGAATTTGGCTGTTGTGAGTGAAGCATATGATCGTTGTGGCG	697
DB	517 CCGATATACCTATTTCGGGGGAATTTGGGCTTTGTGAGTGAAGCATATGATAGGTGTGGTG	576
QY	698 AAGTATGTGCAGAGTATGCAAAAGACATTTTACTTTAGGAACCAAGCTAATGACCCAGAGA	757
DB	577 AAGTATGTGCAGAGTATGCAAAAGACGTTTAACTTTAGGNACTATGCTAATGACTCCCAGAGA	636
QY	758 GAAGAAGAGCTPATCTGGGCAATATATGTGTGGTGCAGAGAACGGATGAGCTTGTGATG	817
DB	637 GAAGAAGGCTPATCTGGGCAATATATGTGTGGTGCAGAGAACAGATGAACCTTCTTGATG	696
QY	818 GCCCTAATGCATCCACATACCTCCGACGCTTTAGATAGTGGGAGCACAGGCTGGAAG	877
DB	697 GCCCAAGCGCATATATTTACCCCGCAGCTTAGATAGTGGGAAATAATAGGCTAGAAG	756
QY	878 ATATTTTCAGTGGCGGCATTTGATATGCTGTGATGCTGCTTTATCCGATACTCTCCA	937
DB	757 ATGTTTCAATGGCGGCCATTTGACATGCTCGATGTTGCTTCTCGATACAGTTCTTA	816
QY	938 GATTTCTGTTGATATTACGCCATTTCAGAGATATGATTGAAGGAATCGGTATGGACTTGT	997
DB	817 ACTTTCAGTTGATATTACGCCATTTCAGAGATATGATTGAAGGAATCGGTATGCACITGA	876
QY	998 GGAATCCAGATACAAAACCTTCGATGAGCTATATCTCTATTGTTACTATGTTCTCGTGA	1057
DB	877 GAAATCGAGATACAAAACCTTCGACGACTATACCTTTATTTGTTATTTATCTGCTGTA	936

QY 1058 CTGTAGGATTGATGAGTGTTCACAGTTATGGGTATTCACCTGAATCAAAAGGCAACAACAG 1111

DB 937 CGGTGGGTTGATGAGTGTTCACAAATATGGGTATCGCCCTGAATCAAAAGGCAACAACAG 996

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DB 997 AGACGATATAATGCTGCTTTGGCTTGGGATCGCAATCAATTAACATACTACTCA 1056

QY 1178 GAGATGTAGGAGAGATGCCAGAGAGAGAGATATCTGCTCAAGATGAATAGCAC 1237

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QY 1705 ACATCATCAAAACCTCAAGTGAG 1728

DB 1597 ACTTATCTCAACTCCTTTTGAGAG 1620

RESULT 6
LERIPE LOCUS LERIPE Tomato fruit ripening specific mRNA. linear PLN 11-MAY-1991

DEFINITION Y00521
ACCESSION Y00521
VERSION Y00521.1 GI:19340
KEYWORDS unidentifed reading frame.
SOURCE Lycopersicon esculentum.
ORGANISM Lycopersicon esculentum.

REFERENCE 1 (bases 1 to 1614)
AUTHORS Bird,C.R.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1987) Bird C.R., Imperial chemical industries PLC, plant biotechnology group, Po Box 11, The Health, Runcorn, Cheshire, WA7 4QE, U.K.

REFERENCE 2 (bases 1 to 1614)
AUTHORS Ray,J., Bird,C., Maunders,M., Grierson,D. and Schuch,W.
TITLE Sequence of pTOM5, a ripening related cdna from tomato
JOURNAL Nucleic Acids Res. 15 (24), 1058 (1987)

tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 1239)
Drake, C.R., Bird, C.R. and Schuch, W.W.
ENHANCEMENT OF GENE EXPRESSION
Patent: WO 9746690-A 2 11-DEC-1997;
ZENECA LTD (GB)
FEATURES
Location/Qualifiers
1..1239
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/clone="GTOM5 - PHYTOENE SYNTHASE GENE"
BASE COUNT 377 a 207 c 317 g 338 t
ORIGIN
Query Match 46.9%; Score 811.2; DB 6; Length 1239;
Best Local Similarity 79.0%; Pred. No. 6.5e-190;
Matches 1035; Conservative 0; Mismatches 203; Indels 72; Gaps 3;
QY 250 ATGTCCTGCTTGGTGGGTTGTTTCCACATCCGAGGTCTCGAATGGGACAGA 309
DB 1 ATGTCCTGCTTGGTGGGTTGTTTCTC---CTTGTGACGCTCAAAATGGGACAGT 57
QY 310 TTGCTGGATTCACTCCGAGAGAAACCCGCTCTTTGTATCATCCAGGTTCTAGTCTCA 369
DB 58 TTAGGAATCACTGCGGGAGGAAACCGTTTTTGTATTCGAGG-----105
QY 370 GATAGGAATTTGATGGGAGTGGGAGATCAAGAAAGTGGGAGACAAAGGTTGGAATTT 429
DB 106 CATAGGAATTTGGTCCATGAGAGATCAATAGAGT-----144
QY 430 GGCTCTTAATTCGTCACCAAGATATTCAGTCTGGTGGATCAAGAACTGAAAGGGA 489
DB 145 -----GGTGGAAAGCAAACTAATAATGGA 168
QY 490 AGCACTTCTCTGTACAGTCCAGTTGGTGGCTAGCCAGCTGGAGAAATGACTGTGCTCA 549
DB 169 CGGAATTTCTGTACGGTCTGCTATTTGGCTACTCCATCTGGAGACGGAGATGACA 228
QY 550 TCAGAGAAAAGGTGATGATGGTATTAAAGCAGCAGCTTTAGTGAAGAGCGCAGCTG 609
DB 229 TCGGAACAGATGGTCTATGATGGTCTTGGAGCAGCAGCTTGTGGAGAGGCAACTG 288
QY 610 AGATCTACCATGATTTAGAGTGAAGCGGATGATGTTGTTCCAGGGGAATTTGGGCTTG 669
DB 289 AGATCTACCAATGATTTAGAGTGAAGCGGATGATGTTGTTCCAGGGGAATTTGGGCTTG 348
QY 670 TTGAGTGAAGCATATGATCTGTCGGAGTATGTCGAGATGTCGAAGCATCAAGCATTTTAC 729
DB 349 TTGAGTGAAGCATATGATGTTGGTGAAGTATGTCGAGATGTCGAAGCATTTTAAAC 408
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DB 409 TTAGGAACCTATGCTATGATCTCCGAGAGAAAGGCTATCTGGGCAATATATGTTAGG 468
QY 790 TGCAGGAGACGATGAGCTTTGATGGCCCTTAATGATCCACATCAACTCCGCAAGCT 849
DB 469 TGCAGAGAACAGATGAACATTTGTTGATGGCCCAAGCAGCATATATACCCGGCAGCC 528
QY 850 TTAGATAGTGGGAGACCGCTGGAGATATTTTCACTGGGCGGCCATTTGATATGCTT 909
DB 528 TTAGATAGTGGGAAATAGGCTAGAGATGTTTCAATGGGCGGCCATTTGACATGCTC 588
QY 910 GATGCTGCTTATCCGATAGTCTCCAGATTTTCCCTGTTGATATTCAGCCATTTCAGAGAT 969
DB 589 GATGGTCTTTGTCGATACAGTTTCTTAATTTCCAGTTGATATTCAGCCATTTCAGAGAT 648
QY 970 ATGATGGAAGATTCGCTATGAGCTTGTGGAATTCAGATACAAACTTTTCGATGAGCTA 1029
DB 1000 -----105

QY	549	ATCAGAGAAAAAGGTGTATGATGTGGTATTAAAGCAGCGAGCTTTAGTGAAGAGGACGCT	608
Db	236	ATCGGAACAGATGGTCTATGATGTGGTATTGAGCAGCGCAGCTTGGTGAAGAGGCAACT	295
QY	609	GAGATCTACCGGATGATTAGAGTGAAGCGGATATTCTGTTCACGGGAATTGGGCTT	668
Db	296	GAGATCTACCAATGAGTTAGAGTGAAGCCGATATACCTATTCCGGGGAATTGGGCTT	355
QY	669	GTTGAGTGAAGCATATGATCTGTTGGCGAAGTAGTGTGCAGAGTATGCAAGACATTTTA	728
Db	356	GTTGAGTGAAGCATATGATAGTGTGGTGAAGTAGTGTGCAGAGTATGCAAGACGTTAA	415
QY	729	CTTAGGAACCAAGCTAATGACCCAGAGAGAAGAGAGCTATCTGGGCAATATATGTGTG	788
Db	416	CTTAGGAACCTATGCTAATGACTCCCGAGAGAAGAGGCTATCTGGGCAATATATGTATG	475
QY	789	GTCGAGAGAAGCGGATGAGCTGTGTATGGCCCTAATGCATCCACACATAACTCCGCAAGC	848
Db	476	GTCGAGAAGAAGATGAACTTGTGTATGGCCCAAGCGATCATATATTACCCGGCGAGC	535
QY	849	TTTATGATAGGTGGGAGACACAGGCTCGGAAGATATTTTCAGTGGCGGCACTTTGATATGCT	908
Db	536	CTTAGATAGGTGGGAATAAGCTAGAGATGTTTCAATGGCGGCCATTTGNACATGCT	595
QY	909	TGATGCTGCTTATCCGATACPGTCTCCAGATTTTCCTGTGTGATATTAGCCATTCAGAGA	968
Db	596	CGATGCTGCTTTGTCGATACAGTTTCTAACTTTCCAGTTTGCATATTCAGCCATTCAGAGA	655
QY	969	TATGATTGAAGGAATCCGATGAGCTTCTGGAAATCCAGATACAAAACCTTCGNATGAGCT	1028
Db	656	TATGATTGAAGGAATCGATGGACTTGGAAATTCGAGAAATTCGAGATACAAAACCTTCGACGAAC	715
QY	1029	ATATCTCTATTGTTACTATGTTGCTGGTACTGTAGGATTGTAGTGTTCAGTTATGGG	1088
Db	716	ATACCTTTATGTTATGTTGCTGTGTCAGGTTGGGTGTGATGAGTGTTCCAATTATGGG	775
QY	1089	TATTGCACCTGAATCAAAAGCAACAGAGAGTGTATATAATGCTGCTTTGGCTTTAGG	1148
Db	776	TATCGCCCTTGATCAAAAGCAACAGAGAGGCTATATATGCTGCTTTGGCTCTGGG	835
QY	1149	GCTTGCAAACTCACTAACCAATATACTCAGAGATGTAGGAAAGATGCCAGAGAGGAAG	1208
Db	836	GATCGCAAACTCAATTAACATAAGCATACTCAGAGATGTTGGAAAGATGCCAGAGAGGAAG	895
QY	1209	AGTATATCTTGCCTCTAAGATGAATTAGCAGCAGCGGGCTCTCCGACGAAGACATATTTGC	1268
Db	896	AGTCTACTTGCCTCAAGATGAATTAGCAGCAGCAGGCTCTATCCGATGAAGATATATTTGC	955
QY	1269	TGGAAGATGACTGTATAAGTGGAGGACTTTATGAAGAAAACAATTCAGAGGGCGAGAA	1328
Db	956	TGGAAGGTTGCCGATTAATGGAGAACTTTTATGAAGAAAACAATATACATAGGCGCAAGAA	1015
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Db	1016	GTTCTTTTGATGGCGAGAGAAAGGCGTGACAGAAATTGAGCTCAGCTAGTAGATTCCCTGT	1075
QY	1389	GTTAAACAGCGCTGCTGTTGTATCGGAAGATATTGACGAGATTTGAAGCCCAACGACTACAA	1448
Db	1076	ATGGGCATCTTTGGTCTTCTGCTCCGCAAAATACTAGATCAGATTGAAGCCCAATGACTACAA	1135
QY	1449	CAACTTCACAGGAGGCTTTATGTAAGCAAGCAAGGAGCT	1490
Db	1136	CAACTTCACAGAGAGCATATGTGAGCAAAATCAAAATATGCT	1177

RESULT 11	
AF220218	
LOCUS	1506 bp mRNA linear PLN 11-FEB-2000
DEFINITION	Citrus unshiu phytoene synthase (Psyl) mRNA, complete cds.
ACCESSION	AF220218
VERSION	AF220218.1 GI:6959859
KEYWORDS	.
SOURCE	Citrus unshiu.

ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 1506)
Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
Isolation of a cDNA encoding phytoene synthase from Citrus
Unpublished

REFERENCE 2 (bases 1 to 1506)
Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
Direct Submission
Submitted (30-DEC-1999) Biological Sciences, Korea Advanced
Institute of Science and Technology, 373-1 Kusong-dong, Yusong-gu,
Taejon 305-701, South Korea
Location/Qualifiers
1. .1506
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/cultivar="Miyagawa (early)"
/db_xref="taxon:55188"
/tissue_type="fruit"
/note="authority: Citrus unshiu (Swingle) Marc."

gene 1. .1506
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112. .1422
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MLDAALSDFTWKEPVDIOEPDRMLEGRMDLRKSVKNFDELILYCYVYAGTVGLASV
PVMGIAPDSOATTESYNAAALGIANQLTNILRDGEDARRGRVYLPQDELAQAQGL
DDDFAGEVITKWRNFMKNKIDRRMFFDMANGVETLSEASRPVPMWASLLLRQLD
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BASE COUNT 448 a 271 c 360 g 427 t
ORIGIN

Query Match	40.3%;	Score 696.8;	DB 8;	Length 1506;
Best Local Similarity	71.2%;	Pred. No. 1.3e-161;		
Matches 949;	Conservative 0;	Mismatches 6;	Gaps 2;	
Qy	212	AATGTGTTTTAGACACCGAGGTTCTGTGTTTCATGAGCATGCTGTGCTTTGTTGGG	271	
Db	74	AAATTTCTTTTATCCAAAATAATAATTTTACAGCATGCTGTGTACATGCTGTGGG	133	
Qy	272	TGTGTTCTCCACTTCCGAGGCTCTCGAATGGGACAGGATGTTGTGGATTCAGTCCGAGAA	331	
Db	134	TGTATACCTTAACCTCACAATGTGCCAATGCTTCGGGTTCGTGATTCACTTCAGTAGG	193	
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Qy	452	GATATTCAATGCTTGGTGGATCAGAACTGAAAAGGGAGACACTTCTCTGTACAGTCCA	511	
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RESULT	13
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LOCUS	1773 bp mRNA linear PLN 04-APR-2001
DEFINITION	Citrus x paradisi phytoene synthase mRNA, complete cds.
ACCESSION	AF152892
VERSION	AF152892.2 GI:13542331
KEYWORDS	.
SOURCE	Citrus x paradisi.

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RESULT 14

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LOCUS      E15683
DEFINITION Gentiana lutea mRNA for Phytoene synthase 4, complete cds.
ACCESSION  E15683
VERSION    E15683.1
KEYWORDS   JP 1998084966-A/4.
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 2868)
AUTHORS    Koiba, H., Kobayashi, H. and Yamamura, S.
TITLE      NEW PHYTOENE SYNTHASE GENE

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JOURNAL Patent: JP 1998084966-A 4 07-APR-1998;
COMMENT  IWATE, PREP GOV
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PD       07-APR-1998
PF       17-SEP-1996 JP 1996245107
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CI       N15/09,C07H21/04,C12N9/00/C09B61/00,(C12N9/00,C12R1:91); CC
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ORIGIN
Query Match 40.1%; Score 692.4; DB 6; Length 2868;
Best Local Similarity 73.6%; Pred. No. 1.5e-160;
Matches 949; Conservative 0; Mismatches 311; Indels 30; Gaps 4;

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Db 450 TGGCAATGTTTCTTGGAGCCAAATTCGAGAAAGTTACCATTTTTCG----- 495
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QY 420 GTGGAATTTGCTCTTTAATGCTGATCCAAAGATATTCATGCTGGTGGATCAAGAAC 479
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